

Please amend Claims 1-20, 22-24, and 26-27 as follows:

1. (Amended) An isolated Glutathione-S-transferase (GST) comprising an amino acid sequence having at least about 80% identity with SEQ ID NO:10, wherein said GST does not comprise an amino acid sequence characterized by SEQ ID NO: 36.
2. (Amended) The GST according to claim 1, wherein said GST is capable of conferring resistance or tolerance upon a plant to an herbicide which comprises at least one of fomesafen and acifluorfen.
3. (Amended) An isolated polynucleotide comprising a region which encodes the GST according to claim 1.
4. (Amended) The polynucleotide according to claim 3, wherein said polynucleotide comprises a nucleotide sequence characterized by SEQ ID NO:14.
5. (Amended) An isolated polynucleotide sequence which is complementary to a sequence which binds to the polynucleotide according to claim 3 at a temperature of between about 60°C and about 65°C in 0.3 strength citrate buffered saline containing 0.1% SDS followed by rinsing at said temperature with 0.3 strength citrate buffered saline containing 0.1% SDS, wherein said polynucleotide sequence comprises a region which encodes a GST, and wherein said polynucleotide sequence is not characterized by SEQ ID NO: 38.
6. (Amended) An isolated protein comprising an amino acid sequence having at least about 70% identity with SEQ ID NO:1, wherein said protein is capable of catalyzing an addition of Beta-alanine to gamma glutamylcysteine.
7. (Amended) The protein according to claim 6, wherein said protein exhibits a K_m for Beta-alanine which is less than said protein's K_m for glycine when said K_m for Beta-alanine and said K_m for glycine are calculated using an identical method.
8. (Amended) The protein according to claim 7, wherein said K_m for Beta-alanine is less than or equal to about 0.8 mM and said K_m for glycine is higher than 0.8 mM.

9. (Amended) The protein according to claim 7, wherein said protein comprises an amino acid sequence characterized by at least one of SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, and SEQ ID NO:5.

10. (Amended) An isolated polynucleotide comprising a region encoding the protein according to claim 6.

11. (Amended) The polynucleotide according to claim 10, wherein said polynucleotide comprises a sequence characterized by SEQ ID NO:6.

12. (Amended) An isolated polynucleotide comprising:

(a) a first region comprising a polynucleotide encoding the GST according to claim 1; and

(b) a second region comprising a polynucleotide encoding a protein comprising an amino acid sequence having at least about 70% identity with SEQ ID NO:1, wherein said protein is capable of catalyzing an addition of Beta-alanine to gamma glutamylcysteine.

13. (Amended) The polynucleotide according to claim 12 wherein said first region comprises a polynucleotide encoding an amino acid sequence characterized by SEQ ID NO:10 and said second region comprises a polynucleotide encoding an amino acid sequence characterized by SEQ ID NO:1.

14. (Amended) A DNA construct comprising a plant operable promoter operably linked to the polynucleotide according to claim 3 which is operably linked to a transcription termination region.

15. (Amended) A method of providing a plant which is resistant or tolerant to an agrochemical, the method comprising:

(a) inserting the polynucleotide of claim 3 into a genome of plant material from a plant;

(b) regenerating at least one plant or plant part therefrom;

(c) applying to said plant or plant part a phytotoxic amount of said agrochemical; and

(d) selecting at least one plant or plant part which is resistant or tolerant to said agrochemical.

16. (Amended) The method according to claim 15 wherein the polynucleotide inserted into said plant material encodes an amino acid sequence characterized by SEQ ID NO:10.

17. (Amended) A method of providing a plant which is resistant or tolerant to an agrochemical, the method comprising:

- (a) inserting the polynucleotide of claim 10 into a genome of plant material from a plant which produces a functional GST;
- (b) regenerating at least one plant or plant part therefrom;
- (c) applying to said plant or plant part a phytotoxic amount of said agrochemical; and
- (d) selecting at least one plant or plant part which is resistant or tolerant to said agrochemical.

18. (Amended) The method according to claim 15 wherein said agrochemical comprises at least one of fomesafen and acifluorfen.

19. (Amended) A transgenic plant or plant part obtained according to the method of claim 15.

20. (Amended) The transgenic plant or plant part of claim 19 wherein said plant or plant part is a soybean plant or plant part.

22. (Amended) A method of providing a plant with an additionally desired agronomic trait, the method comprising:

- (a) inserting a polynucleotide which encodes an additionally desired agronomic trait into a genome of plant material from the transgenic plant or plant part of claim 19; and
- (b) regenerating a plant or plant part from said plant material.

23. (Amended) The method according to claim 22 wherein said additionally desired agronomic trait provides resistance to an herbicide which comprises glyphosate or a salt thereof.

24. (Amended) A method of selectively controlling weeds in a field which comprises crop plants and weeds, the method comprising applying to said field an agriculturally acceptable formulation of an agrochemical comprising at least one of fomesafen and acifluorfen wherein said crop plants comprise transgenic plants according to claim 19.

26. (Amended) An isolated protein comprising either an amino acid sequence characterized by SEQ ID NO:10 or an amino acid sequence variant thereof having a Smith Waterman score greater than 766 calculated using a FASTA3 algorithm, wherein said amino acid sequence variant encodes a Glutathione-S-transferase.

27. (Amended) An isolated protein comprising either an amino acid sequence characterized by SEQ ID NO:1 or an amino acid sequence variant thereof having a Smith-Waterman score greater than 2152 calculated using a FASTA3 algorithm, wherein said amino acid sequence variant encodes a homoglutathione synthetase.

Please add Claims 28-41 as follows:

28. (New) An isolated polynucleotide comprising a region which encodes the GST according to claim 2.

29. (New) The polynucleotide according to claim 28, wherein said polynucleotide comprises a nucleotide sequence characterized by SEQ ID NO:14.

30. (New) An isolated polynucleotide sequence which is complementary to a sequence which binds to the polynucleotide according to claim 4 at a temperature of between about 60°C and about 65°C in 0.3 strength citrate buffered saline containing 0.1% SDS followed by rinsing at said temperature with 0.3 strength citrate buffered saline containing 0.1% SDS, wherein said polynucleotide sequence comprises a region which encodes a GST, and wherein said polynucleotide sequence is not characterized by SEQ ID NO: 38.

31. (New) The protein according to claim 8, wherein said protein comprises an amino acid sequence characterized by at least one of SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, and SEQ ID NO:5.

32. (New) An isolated polynucleotide comprising a region encoding the protein according to claim 7.

33. (New) An isolated polynucleotide comprising a region encoding the protein according to claim 8.

34. (New) An isolated polynucleotide comprising a region encoding the protein according to claim 9.

35. (New) A DNA construct comprising a plant operable promoter operably linked to the polynucleotide according to claim 4 which is operably linked to a transcription termination region.

36. (New) A DNA construct comprising a plant operable promoter operably linked to the polynucleotide according to claim 5 which is operably linked to a transcription termination region.

37. (New) A DNA construct comprising a plant operable promoter operably linked to the polynucleotide according to claim 10 which is operably linked to a transcription termination region.

38. (New) A DNA construct comprising a plant operable promoter operably linked to the polynucleotide according to claim 11 which is operably linked to a transcription termination region.

39. (New) A DNA construct comprising a plant operable promoter operably linked to the polynucleotide according to claim 12 which is operably linked to a transcription termination region.

40. (New) A DNA construct comprising a plant operable promoter operably linked to the polynucleotide according to claim 13 which is operably linked to a transcription termination region.

41. (New) A method for providing a plant with an additionally desired agronomic trait, the method comprising:

- (a) crossing the transgenic plant or plant part of claim 19 with a plant which expresses an additionally desired agronomic trait; and
- (b) selecting a transgenic plant resulting from part (a) which expresses said additionally desired agronomic trait.

REMARKS

The specification is amended herein to include the continuing data on the first page. The claims have been amended to better conform them to U.S. practice and to eliminate multiple dependency. The paper copy of the Sequence Listing has been amended to correct minor formatting errors. Additionally, an initial computer readable form (CRF) of the Sequence Listing is submitted herewith. No new matter has been added.

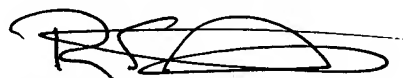
The Examiner is respectfully requested to enter the above amendments prior to calculating the claim fees and initiating substantive examination of the application on the merits. After entry of the above amendments, Claims 1-20, 22-24, and 26-41 (4 independent claims, 39 total claims) are pending in the application.

Attached hereto is a marked-up version of the changes made to the claims by the current amendment. The attached marked-up pages are captioned "**Version With Markings To Show Changes Made**".

Syngenta Biotechnology, Inc.
Patent Department
P.O. Box 12257
Research Triangle Park, NC 27709-2257

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Respectfully submitted,



Randee S. Schwartz
Attorney for Applicants
Reg. No. 45,085
(919) 765-5098